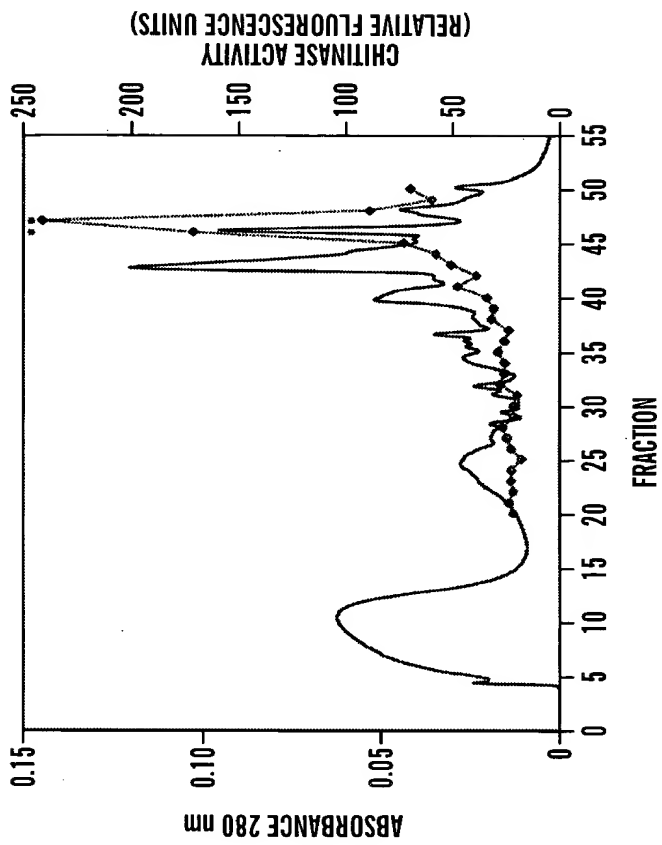


**FIG. 1A**



**FIG. 1B**



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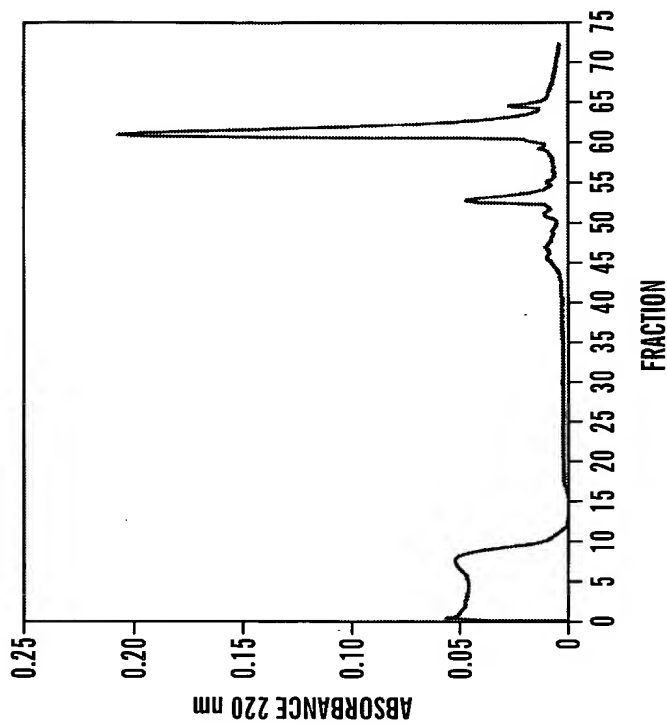


FIG. 1D

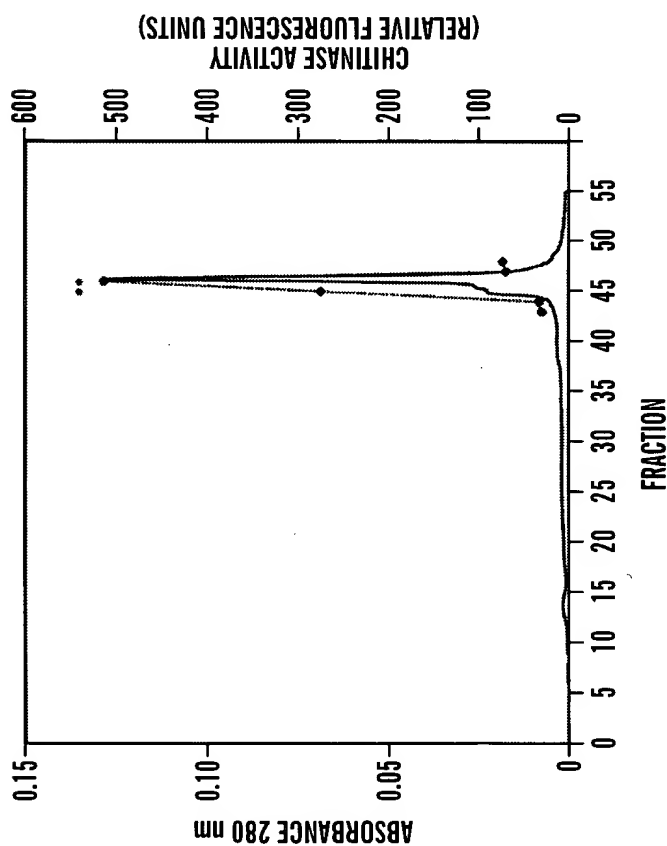


FIG. 1C

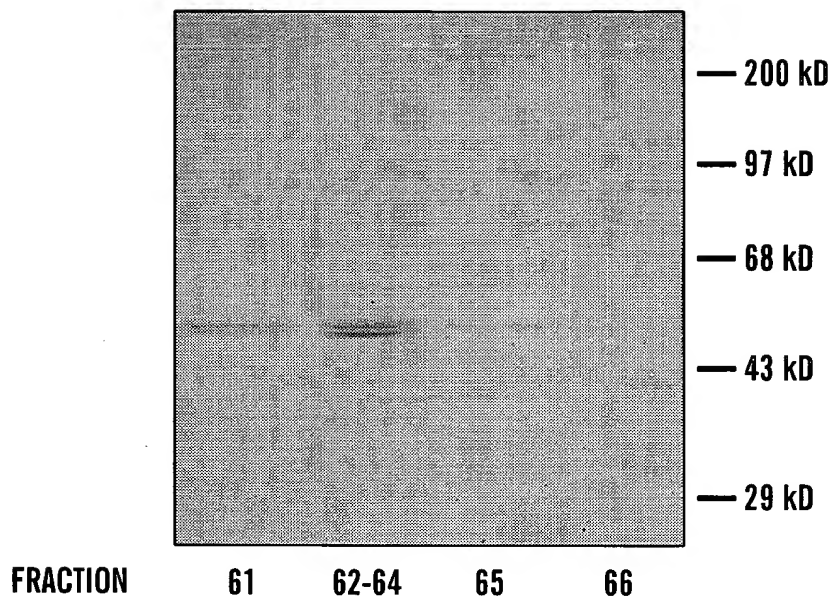


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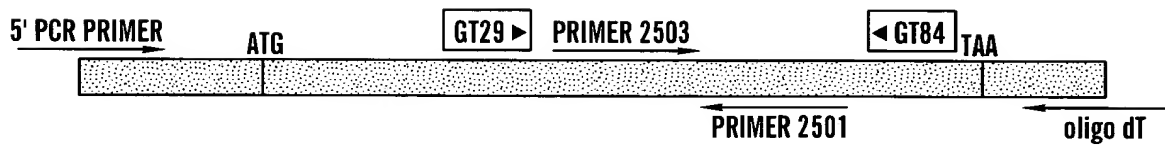
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**FIG. 1E**



**FIG. 2**

**FIG. 3**

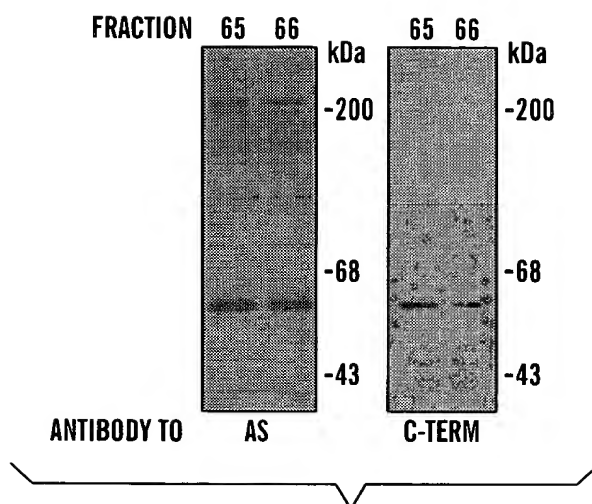


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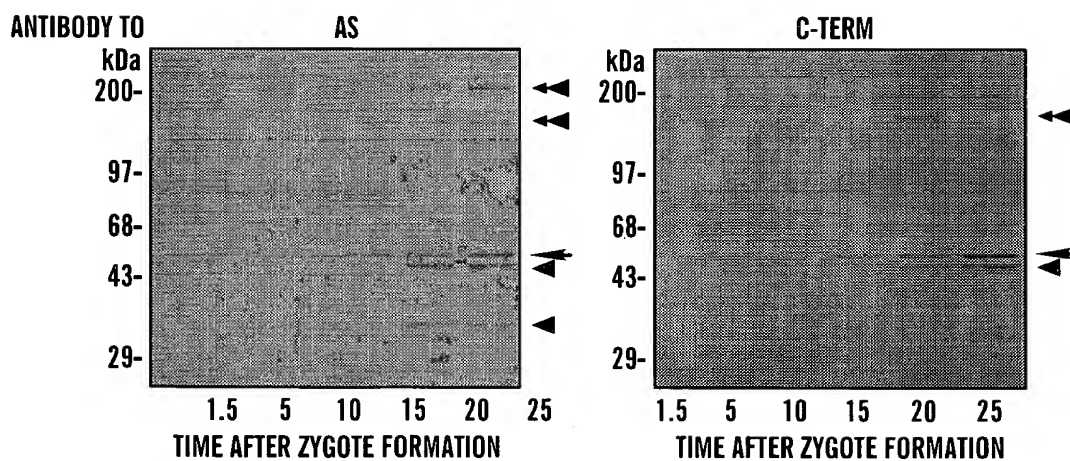
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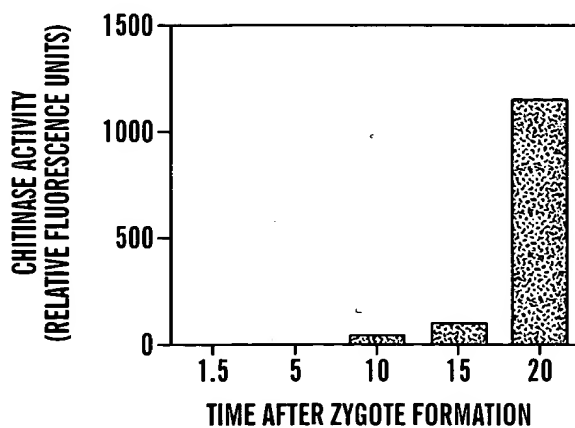
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**FIG. 4A**



**FIG. 4B**



**FIG. 4C**

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FIG. 5C

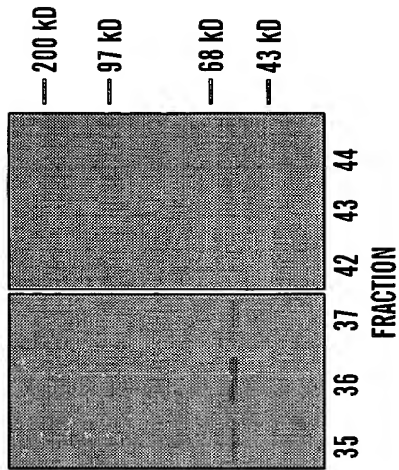


FIG. 5E

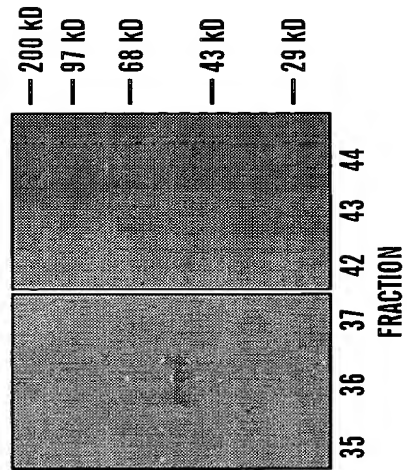


FIG. 5B

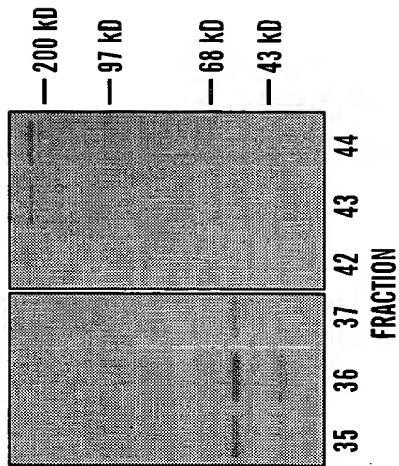


FIG. 5D

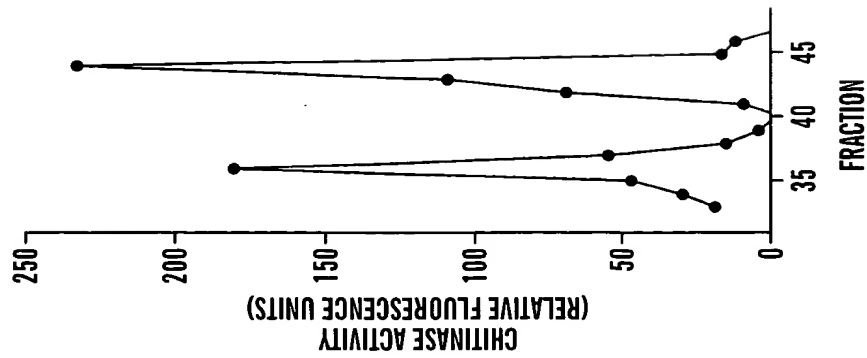
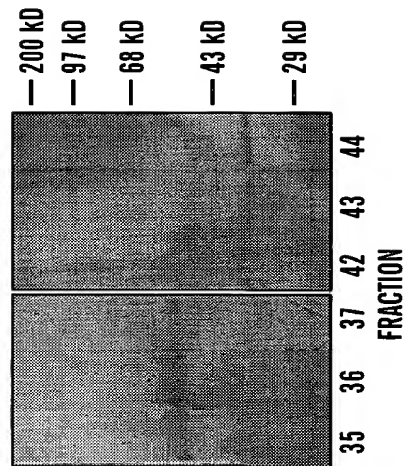


FIG. 5A

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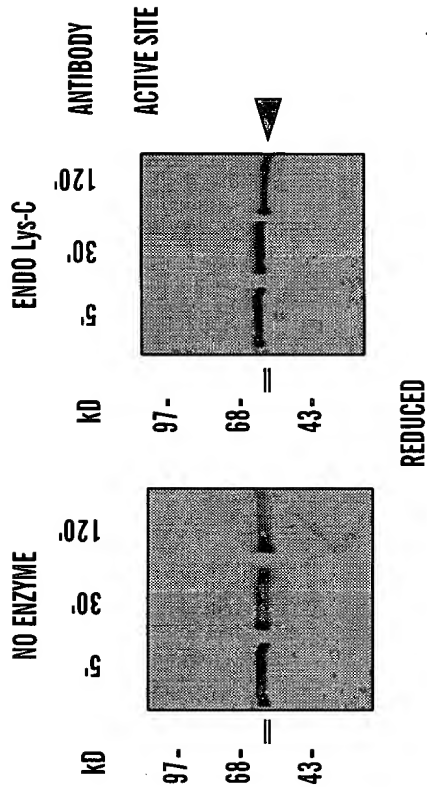


FIG. 6B

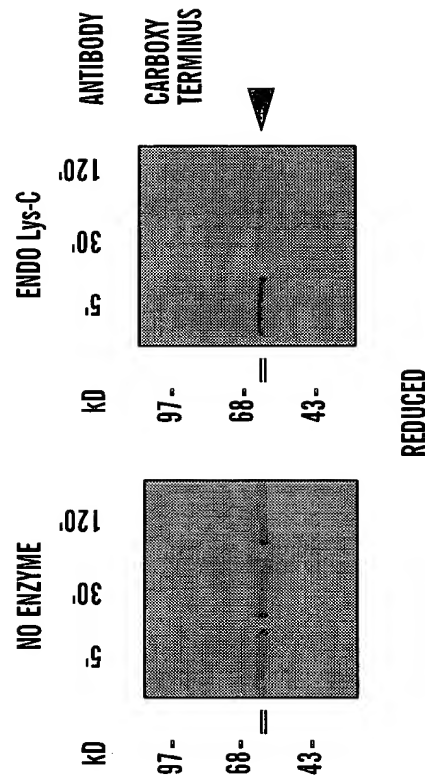


FIG. 6C

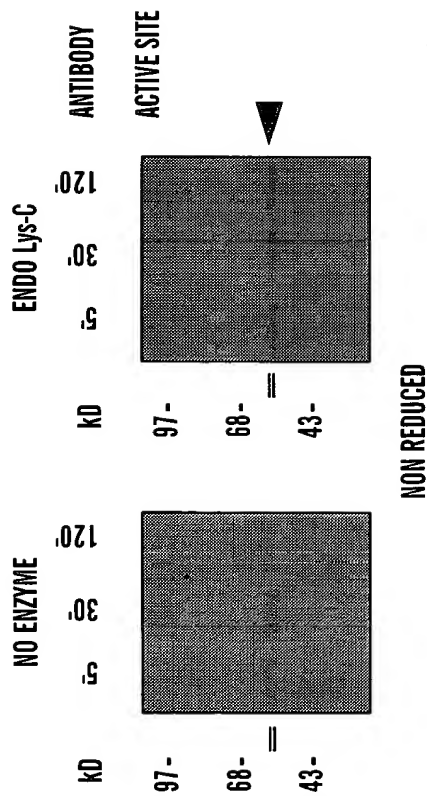


FIG. 6D

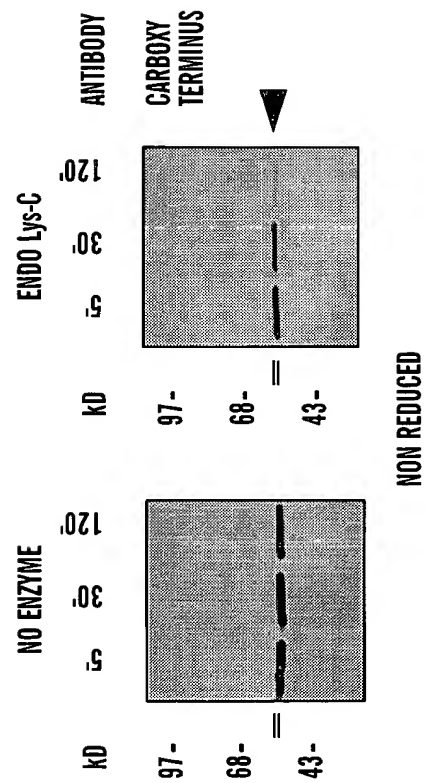


FIG. 6E

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FIG. 7A

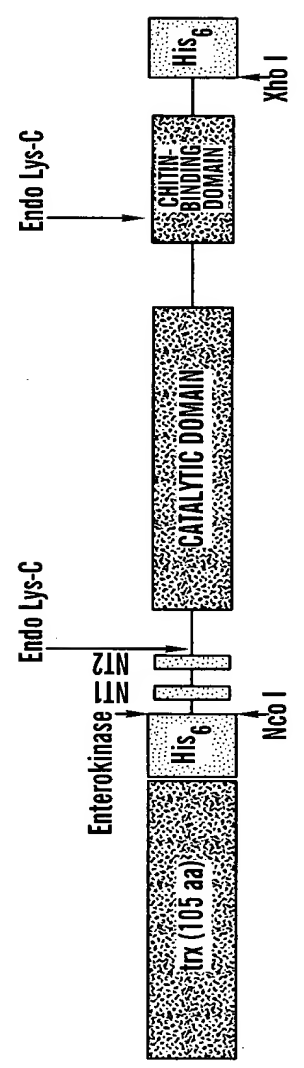


FIG. 7B

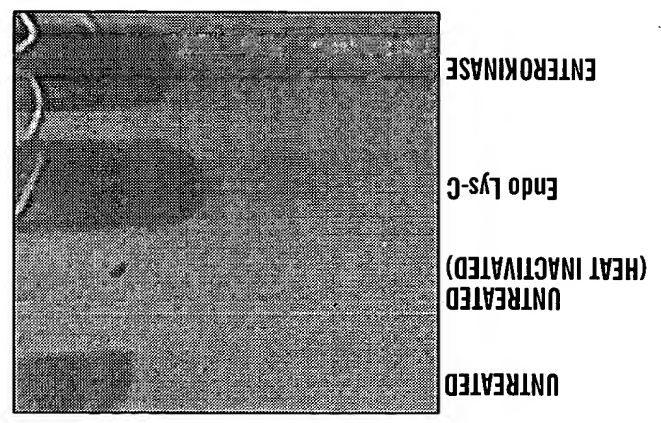
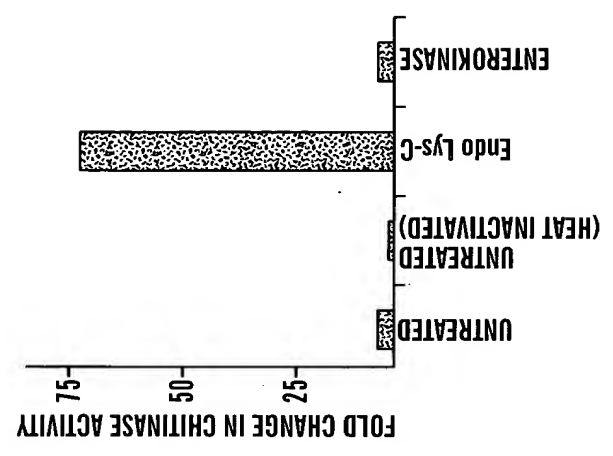


FIG. 7C





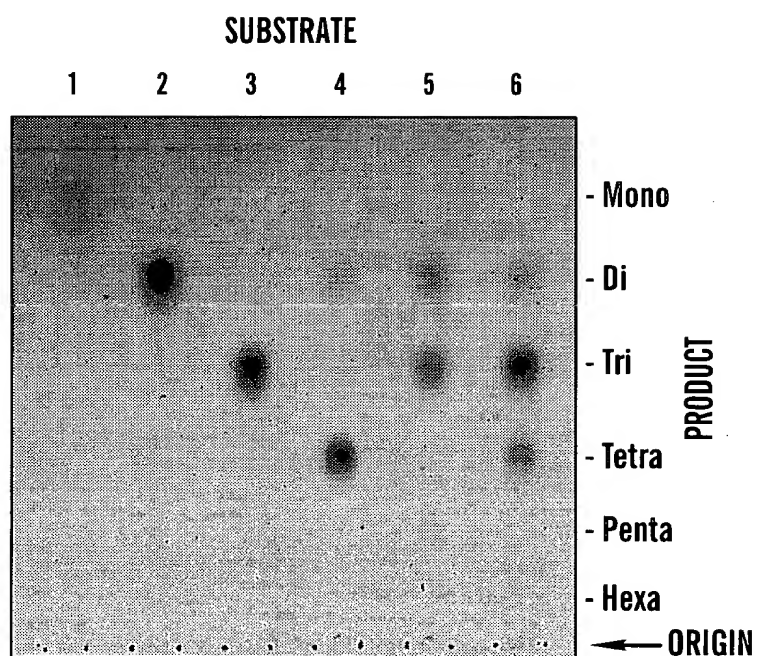


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***FIG. 8***



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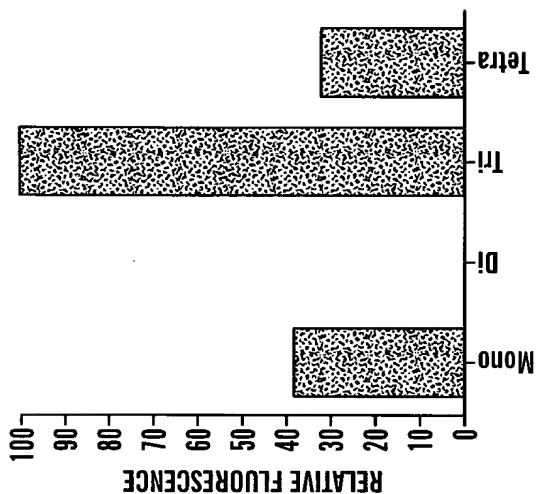


FIG. 9B

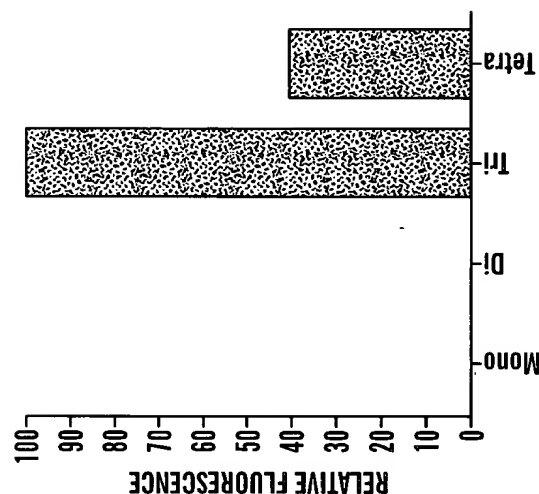


FIG. 9D

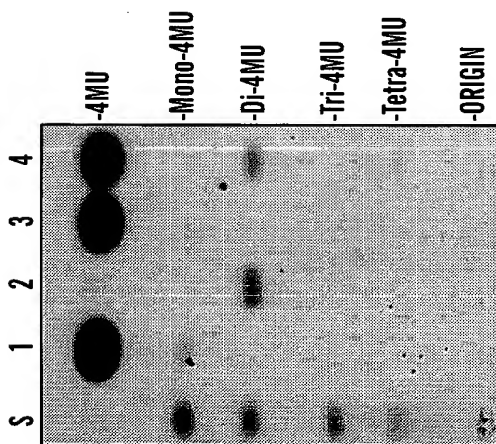


FIG. 9A

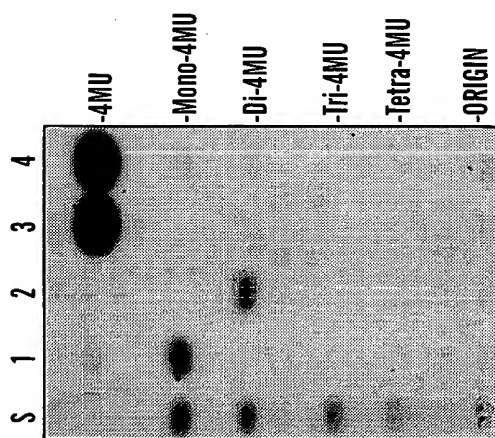


FIG. 9C



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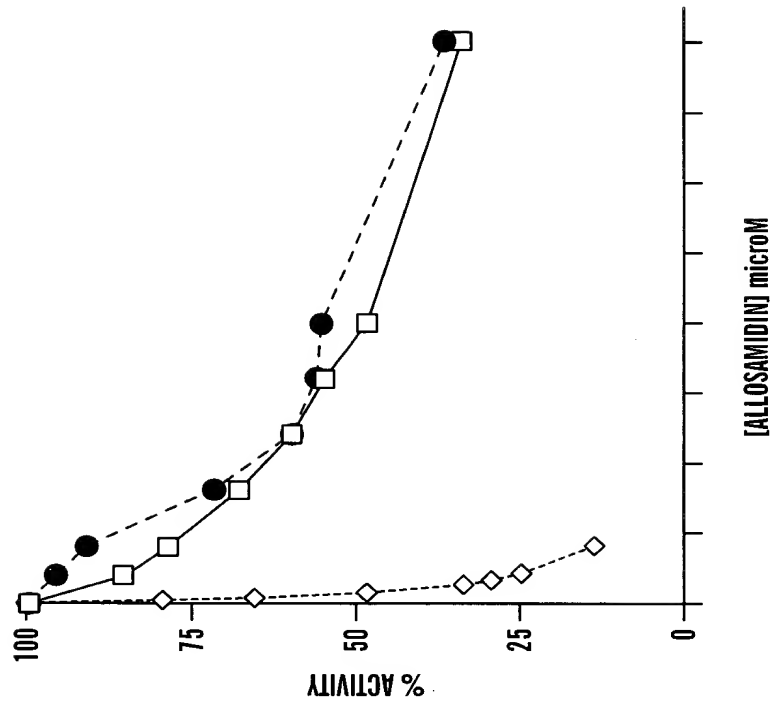


FIG. 10B

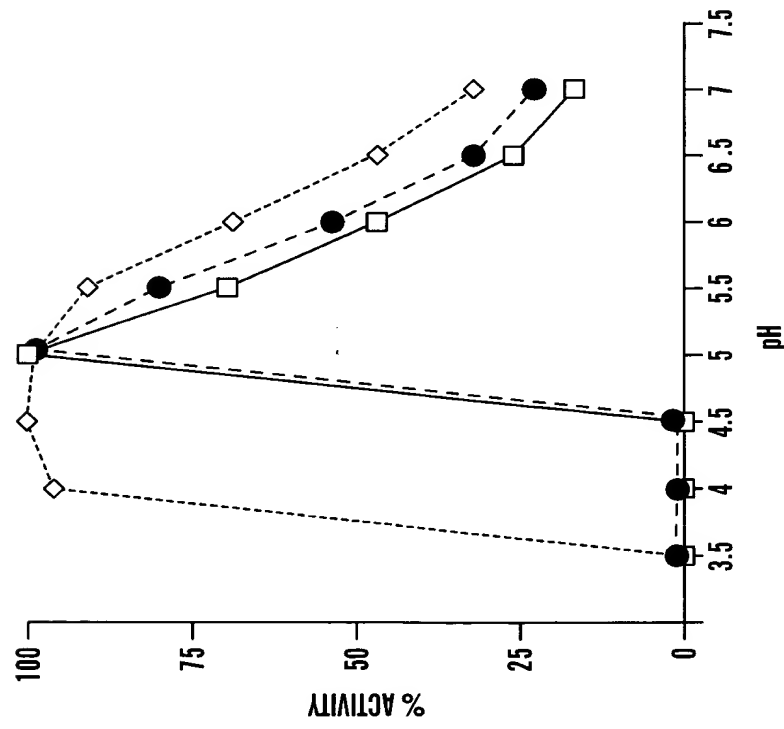


FIG. 10A



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FIG. 11

PfCHT1 MNFTVKGSEFLVICLACCLSTVSVIRG----- 28  
PgCHT1 MNFKISLFLIVSLYSANSRT-----LGGNNINNSLGLIRENQKTHOTETHEHESFSLKSNNSNFTVE 64  
Pro-enzyme domain

PfCHT1 HRARPGESE-----KN-----Catalytic domain begins  
PgCHT1 -----YGSYCGDGCNSRITQNNQININQNDKSPQILEEYCKKQGIAGYYGSWNSQDDRAKEMI 125  
NT1 NT2 Substrate-binding site

PfCHT1 --NPNLNVVHMSPAQODLSYDSIESIVGSPLLFKSLIGLEYIGLNEYFNDAMNLRKARPDIMLLSLGGE 140  
PgCHT1 DSNPMVSILYIAPARINMLYDVSRRPFNGRQRFLLRKHGLEYYETYGMLNBEIRIRKVRPDVILLSLGGE 195  
Active site

PfCHT1 TYHPSSFDSALNAVEKIANLVDELGFDGIDVDYEPNGSFDGLNDKBEKADFFVQYVTKLREYMCDDKLISI 210  
PgCHT1 TYM-IDIEKEIDYVDKILQVNDFDLGVDIDWEPHGKPFYNLBNLFSNYIKLINLLAKTIPEEKLISI 264

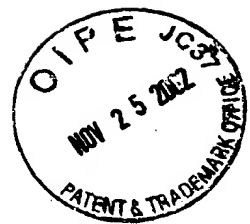
PfCHT1 SQSSNGALSCI-GFNDPKKICDDEAPYNSKYFNKP-DVKKELLRAAQMASAGGAIYLAANNLKMIDMVF 278  
PgCHT1 SGSSNAALSVCVSGVAS---PCDDESPYNTKFLSEBQIETNKEHLRAAAMLSAGTFINIFNTAKEKIDLVF 331

PfCHT1 VQTFNYTNSDSTVMGBLYDSYAYGKCYDYVVIIMGFTLMFPSTPPNPNDDKMLVKSIGDFVKTKENKLNKR 348  
PgCHT1 IQOTNL-ETTNPDIHVDNYLSHLYPGLKNITIIIGFSLEHNRGQSPENKELLELVGKTIHDKNQNNR 400

Catalytic domain ends

PfCHT1 ADGPGWLSSLSSDNAHNEQLAIEYFVESLH. 378  
PgCHT1 ADGIGIMHLFMKBQLPTGSDVDIFLTNIMWHLNPEVQTPKDLTITENPEDCSTIDEYVPGLVIPITIGIN 470  
Chitin-binding domain begins

PfCHT1 DYYTHAIWKTRSYSIHAPGVDRYENDLVKVCYEKICDGKAANYNTDYKESSIIIMKGBPYLIKHWQQGP 540  
PgCHT1 PEGQALSYTKLDASKCPGIEBNKCYPKPLEVEEQYEQEVDLPQ. 587



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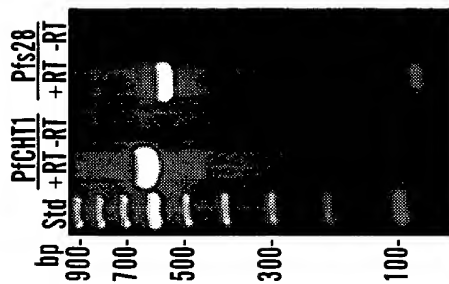


FIG. 12C



FIG. 12B

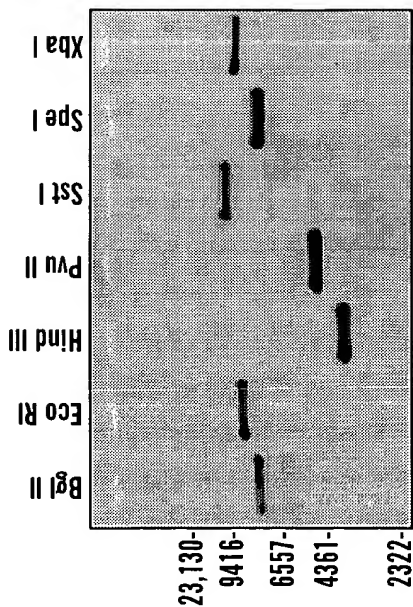
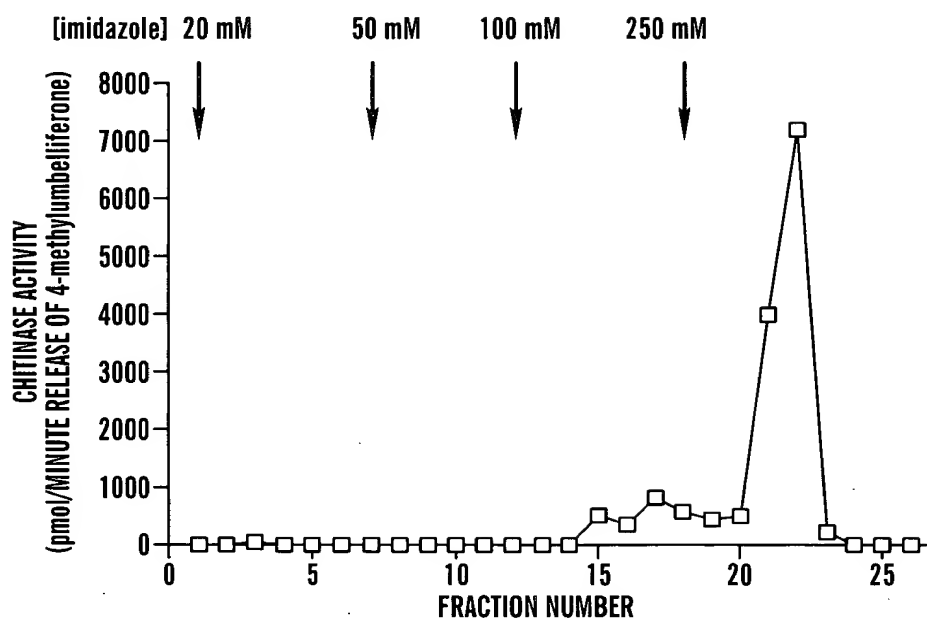


FIG. 12A

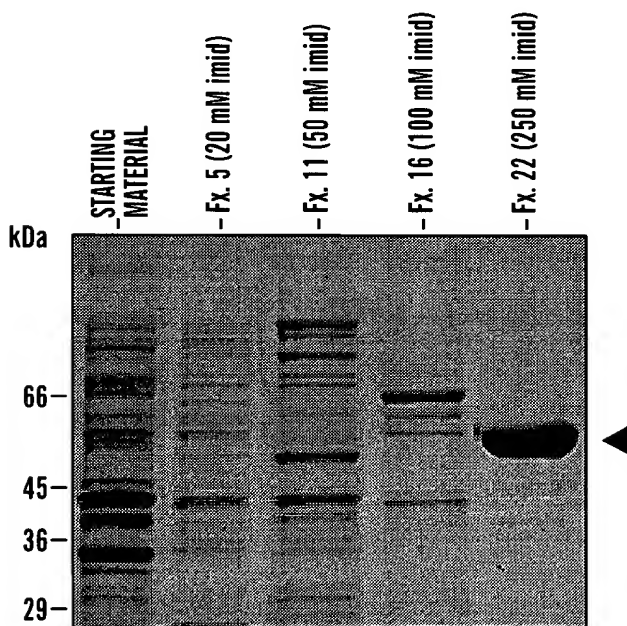


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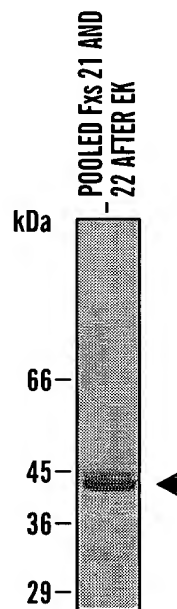
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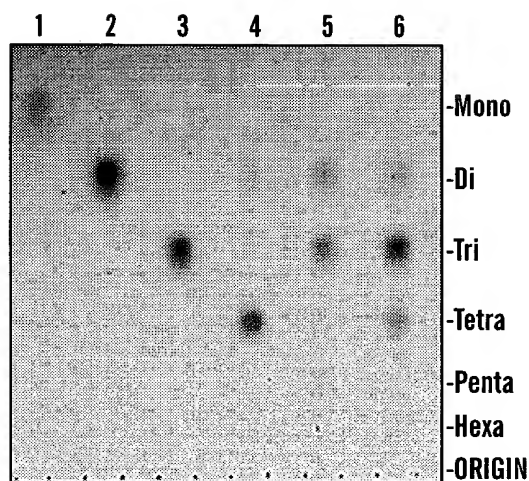
**FIG. 13A**



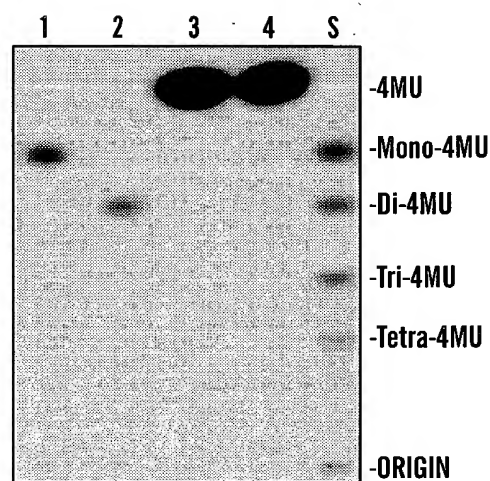
**FIG. 13B**



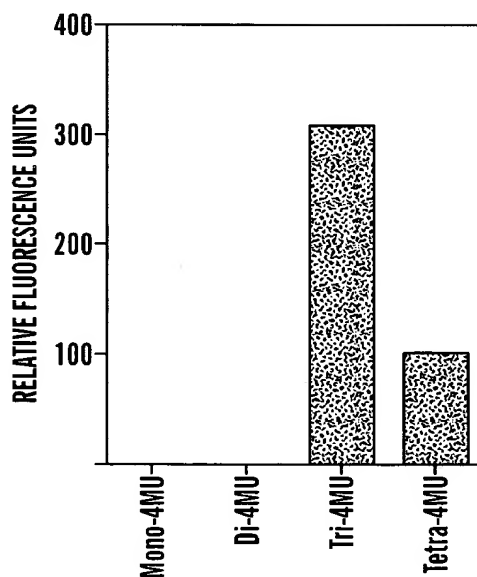
**FIG. 13C**



**FIG. 14A**



**FIG. 14B**



**FIG. 14C**

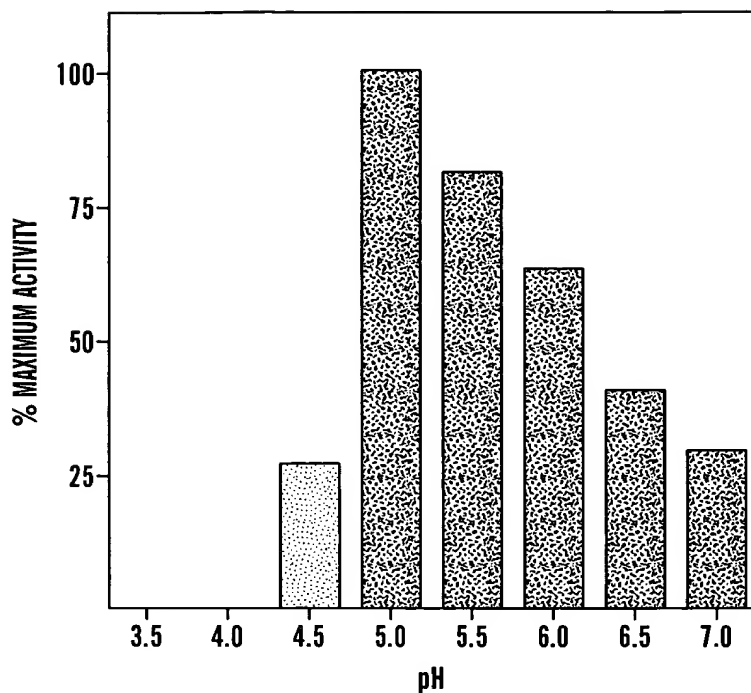


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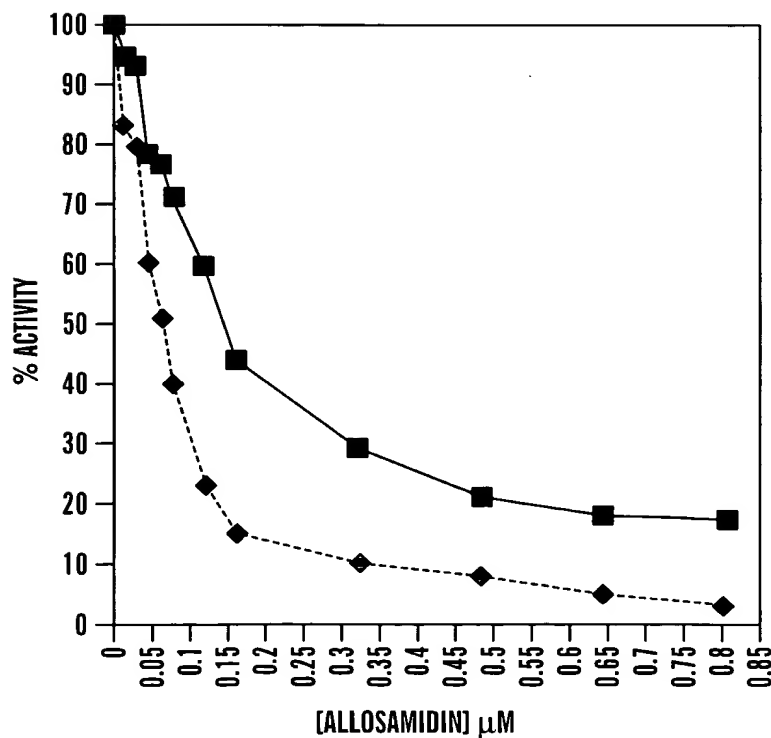
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**FIG. 15A**



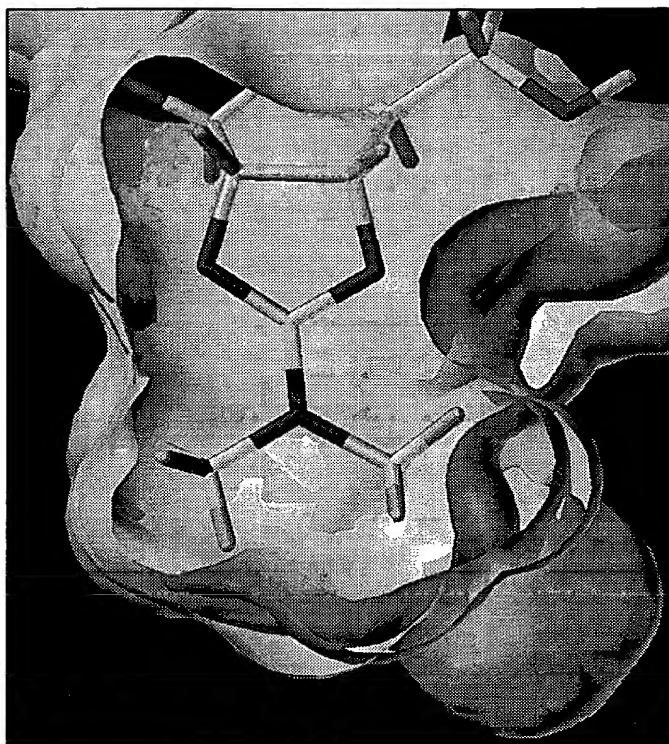
**FIG. 15B**





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**FIG. 16**